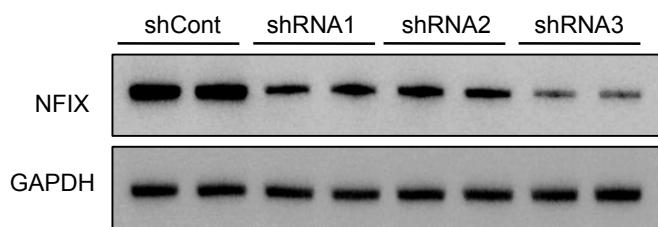
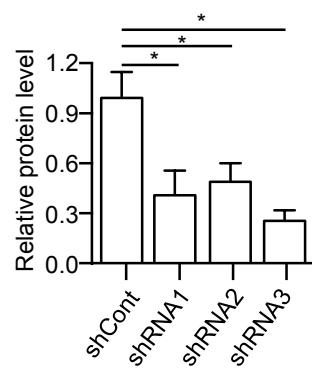


A**B****Figure S1. Knockdown of NFIX by shRNAs in U87 cells.**

(A) Immunoblotting analysis of NFIX and GAPDH in U87 cells expressing shRNAs targeting human NFIX. Representative images are shown. (B) The bar chart is relative expression level of NFIX normalized with GAPDH ($n=6$). All data are represented as the mean \pm s.e.m. * $p<0.05$ (Student's t test).

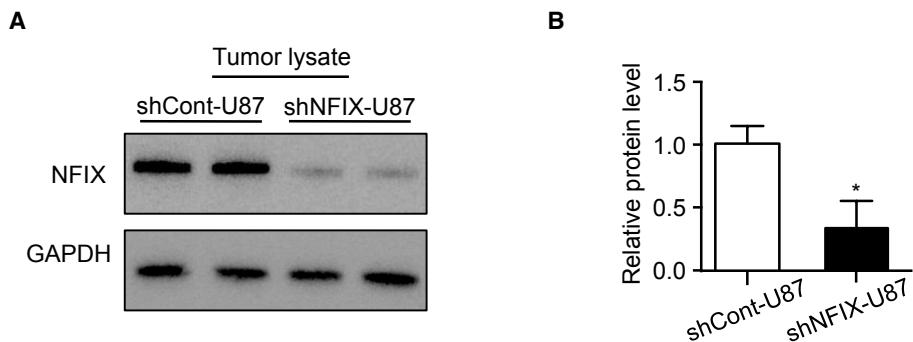
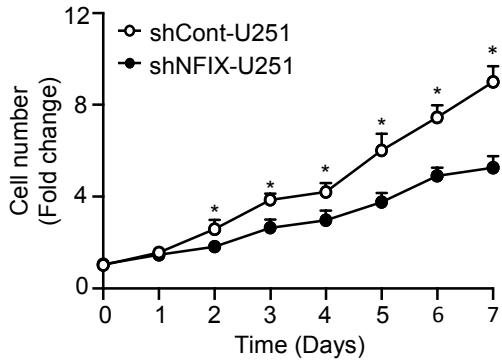
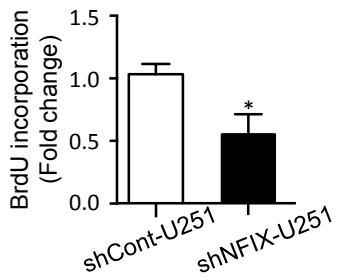
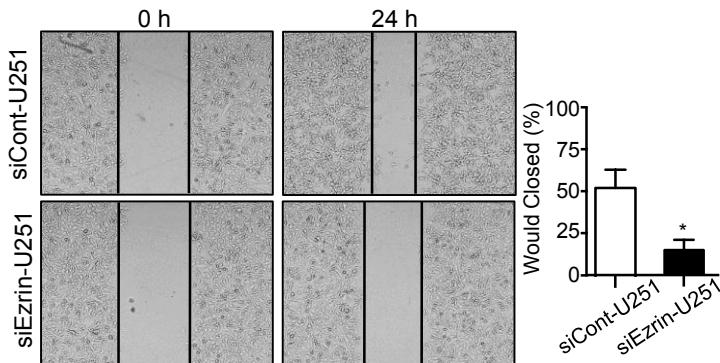
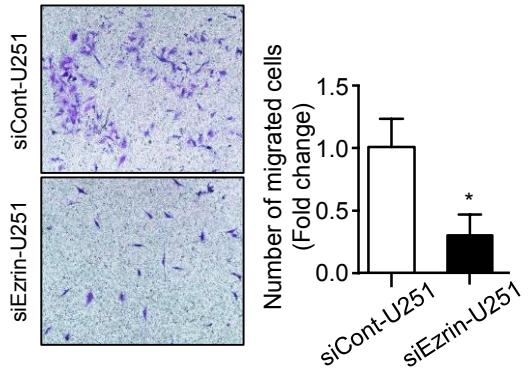


Figure S2. Decreased expression of NFIx in orthotopic tumors.

(A) Immunoblotting analysis of NFIx and GAPDH in orthotopic tumors of nude mice implanted with U87 cells stably expressing shNFIx or control shRNA. Representative images are shown. (B) The bar chart is relative expression level of NFIx normalized with GAPDH ($n=6$). All data are represented as the mean \pm s.e.m. * $p<0.05$, shCont-U87 vs. shNFIx-U87 (Student's t test).

A**B****C****D****Figure S3. NFIX deficiency inhibits proliferation and migration of U251 GBM cells.**

U251 cells stably expressing shNFIU (shNFIU-U251) or control shRNA (shCont-U251) were used. (A) Cell number was determined by trypan blue assay at indicated time points (n=6). (B) BrdU incorporation of cells (n=6). (C) Wound healing assay of cells was determined at 0 and 24 hours after wound was created. The right panel is the percentage of would closed at 24 hours (n=6). (D) Transwell assays of U251 cells stably expressing shNFIU or control shRNA. The right panel is the quantification of the number of migrated cells (n=6). All data are represented as the mean \pm s.e.m. *p<0.05, shCont-U251 vs. shNFIU-U251 group (Student's t test).

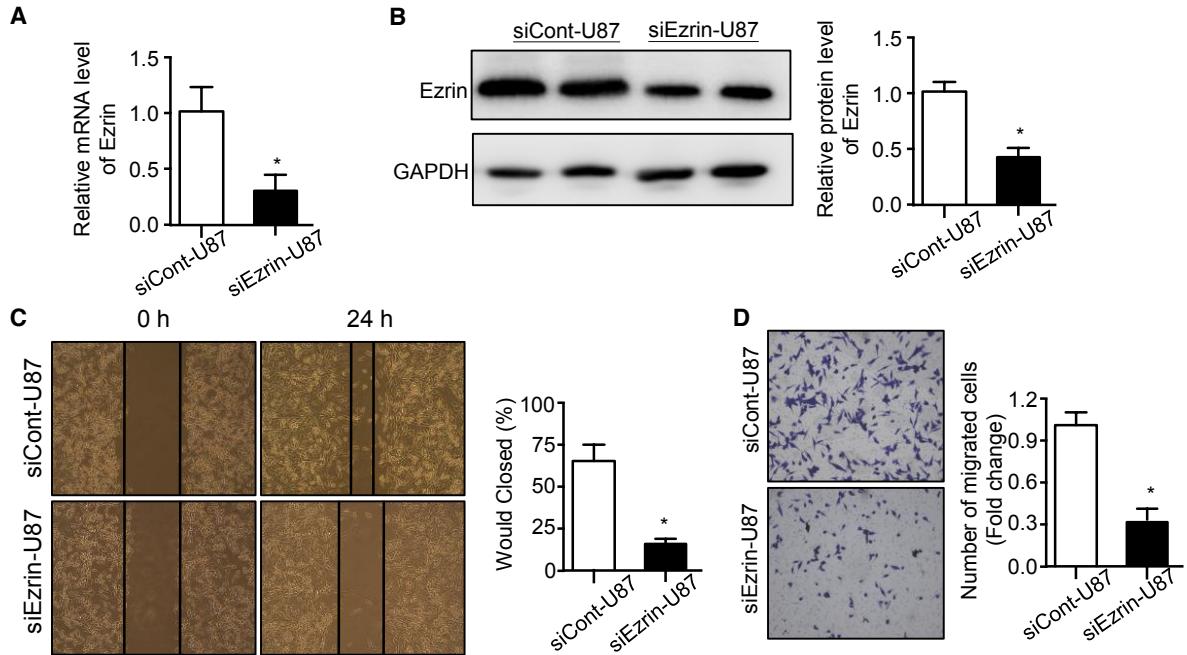


Figure S4. Decreased invasion and migration of U87 GBM cells transfected with siEzrin.

U87 cells were transfected with siRNA against Ezrin (siEzrin-U87 cells) or scramble control (siCont-U87 cells). (A) Relative mRNA levels of *Ezrin* normalized with *GAPDH* in siEzrin-U87 and siCont-U87 cells (n=6). (B) Immunoblotting analysis of Ezrin and GAPDH in siEzrin-U87 and siCont-U87 cells. Representative images are shown. (C) Wound healing assay of cells was determined at 0 and 24 hours after wound was created (n=6). (D) Transwell assays of siEzrin-U87 and siCont-U87 cells (n=6). All data are represented as the mean ± s.e.m. *p<0.05, siEzrin-U87 vs. siCont-U87 group (Student's t test).

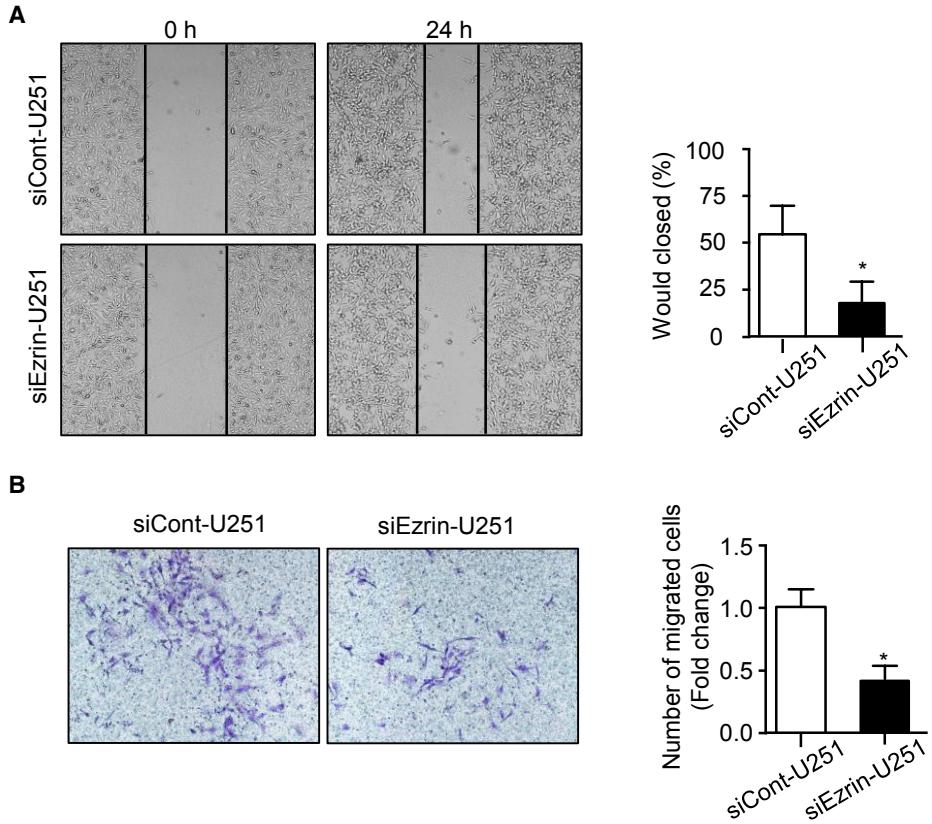


Figure S5. Impaired migration of U251 GBM cells transfected with siEzrin.
 U251 cells were transfected with siRNA against Ezrin (siEzrin-U251 cells) or scramble control (siCont-U251 cells). (A) Wound healing assay of cells was determined at 0 and 24 hours after wound was created (n=6). (B) Transwell assays of siEzrin-U251 and siCont-U251 cells (n=6). All data are represented as the mean \pm s.e.m. *p<0.05, siEzrin-U251 vs. siCont-U251 group (Student's t test).

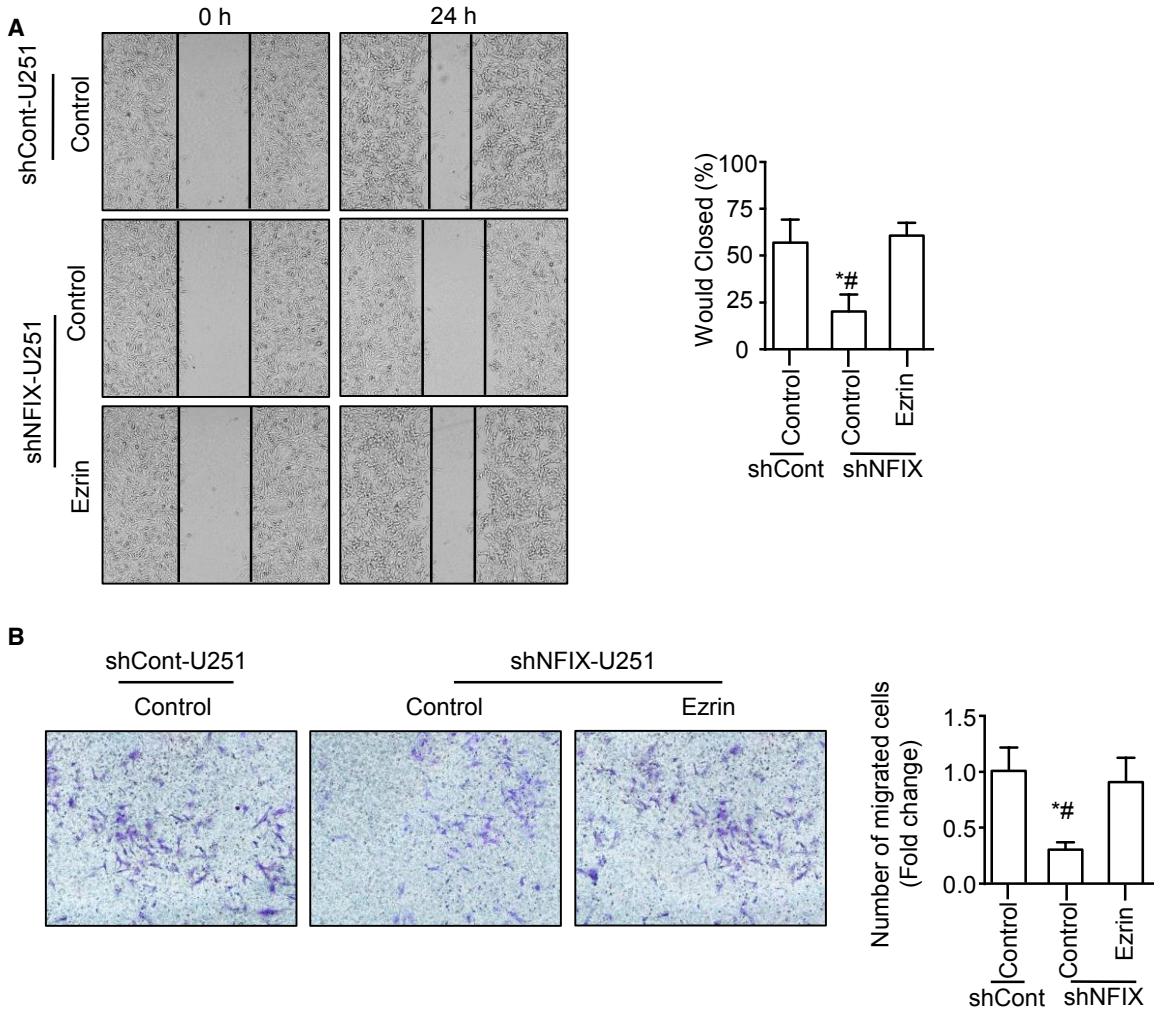


Figure S6. Replenishment of Ezrin reverses defective migration in shNFIx-U251 cells.

shNFIx-U251 and shCont-U251 cells overexpressing Ezrin were generated by lentivirus-mediated overexpression and were subjected to the following experiments. (A) Wound healing assay ($n=6$). (B) Transwell assays ($n=6$). * $p<0.05$, shNFIx+Control vs. shCont+Control; # $p<0.05$, shNFIx+Control vs. shNFIx+Ezrin (One-way ANOVA).

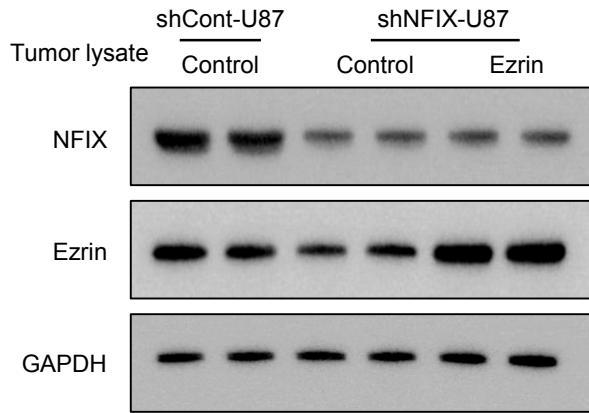
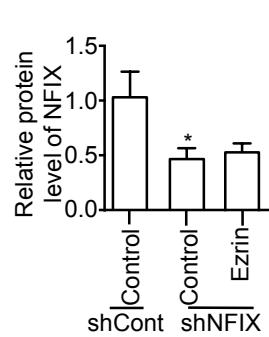
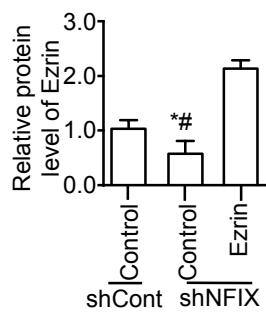
A**B****C**

Figure S7. Protein expression levels of NFIX and Ezrin in orthotopic tumors.

(A) Immunoblotting analysis of NFIX, Ezrin and GAPDH in orthotopic tumors of nude mice implanted with indicated U87 cells. Representative images are shown. (B) The bar chart is relative expression level of NFIX normalized with GAPDH (n=6). (C) The bar chart is relative expression level of Ezrin normalized with GAPDH (n=6). All data are represented as the mean \pm s.e.m. *p<0.05, shNFIU+Control vs. shCont+Control; #p<0.05, shNFIU+Control vs. shNFIU+Ezrin (One-way ANOVA).

Figure 1

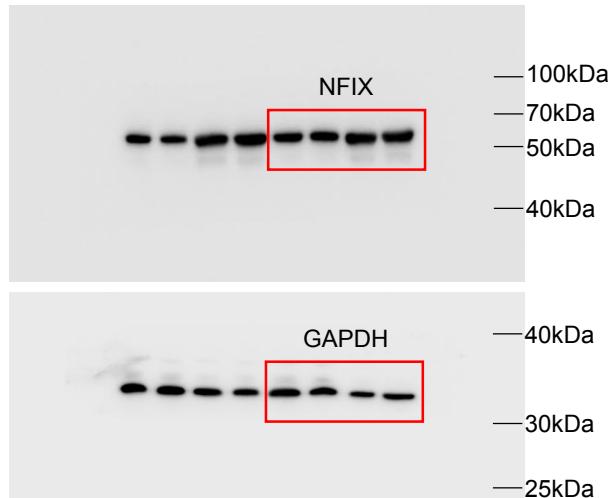


Figure 2

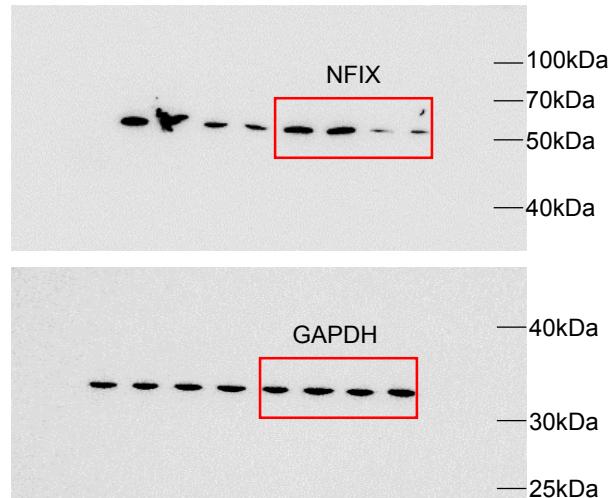


Figure 4

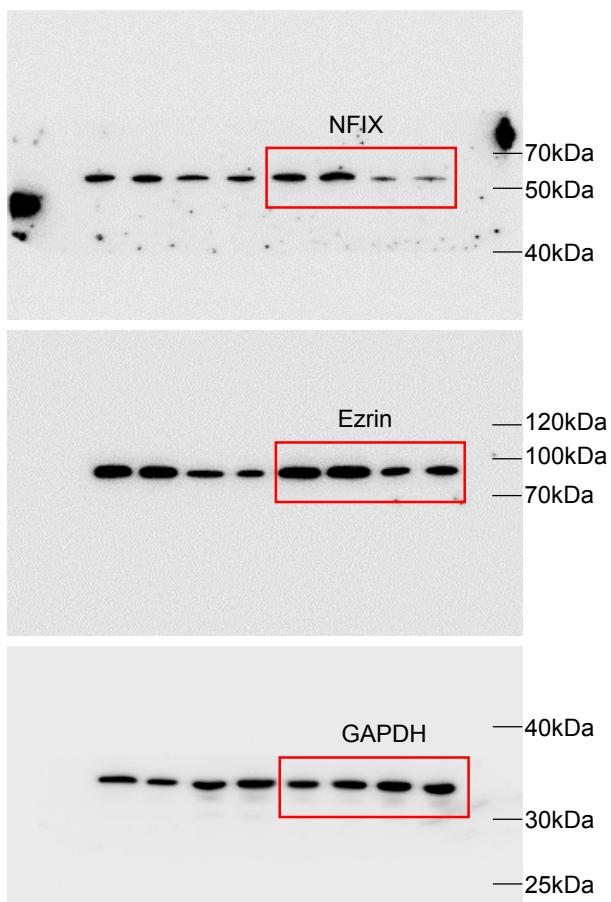


Figure 5

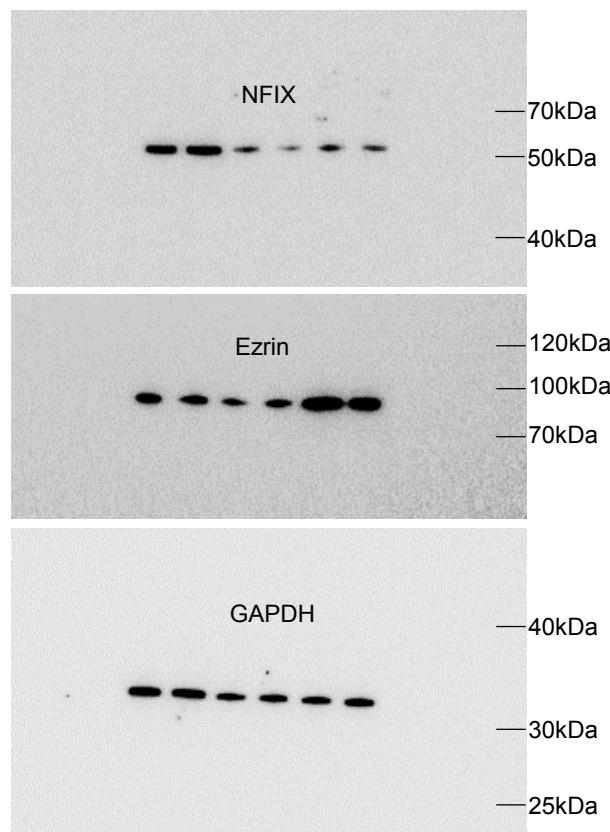


Figure S8. Full images of immunoblotting.

Gene name	Sequences (5' to 3')	
<i>NFIA</i>	Forward	AGCATGAGTCCAGGAGCAAT
	Reverse	TGACTGACTGCCACTCCTG
<i>NFIB</i>	Forward	GCCACAATGATCCTGCCAAGAA
	Reverse	GGTGGAGAACAGACAGAGACCTCTGA
<i>NFIC</i>	Forward	GGACAGGGATGGGCTCTG
	Reverse	CGTTCTTCTGAGGCCAGTGC
<i>NFIX</i>	Forward	CGGCTCTACAAGTCGCCTC
	Reverse	GCAGTGTTTGATGTCCGC
<i>Ezrin</i>	Forward	AGCACACGGAGCACTGCAGG
	Reverse	GTAACTCGGACATTGATTGG
<i>NIFX RE2</i>	Forward	ACCCTCTGATAACAGGTGCCA
	Reverse	TGGGGGCCAGTAGAATTGC
<i>Distal</i>	Forward	TGCATAGAGGAAACCCAGCA
	Reverse	TGGAGGTTGCAGTGAGTCAA

Table S1. Primer sequences for real-time quantitative PCR analysis.

siRNA	Sequences (5' to 3')	
siEzrin	sense	AUCAGGUGGUAAAGACUAU
	antisense	AUAGUCUUUACCACCUGAU
Control	sense	UUCUCCGAACGUGUCACGU
	antisense	ACGUGACACGUUCGGAGAA

Table S2. Sequences of siRNAs.



Cell Line Authentication Service
STR Profile Report

Sample Submitted By: Dr. Zhuohao Liu
Shenzhen Hospital, Southern Medical University
Email Address: lchouhoo@gmail.com
Sales Order: 191220B
Cell Line Designation: U-87MG
Date Sample Received: Dec 20th, 2019
Report Date: Dec 20th, 2019

Methodology: Nineteen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available EX20 Kit from AGCU. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int J Cancer. 2013;132(11):2510-9.

GTB™ performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards.

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NOTE: According to the recommendations of IJC on cell line authentication, the report is valid for 3 years since the issue date.

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Jiangsu, P.R. China



GENETIC TESTING BIOTECHNOLOGY

Cell Line Authentication Service
STR Profile Report

Sales Order: 191220B

Test Results for Submitted Sample			ExPASy Reference Database Profile	
Loci	Query Profile: U-87MG		Database Profile: U-87MG ATCC	
Amelogenin	X			X
D3S1358	16	17		
D13S317	8	11	8	11
D7S820	8	9	8	9
D16S539	12		12	
Penta E	7	14		
TPOX	8		8	
TH01	9.3		9.3	
D2S1338	20	23		
CSF1PO	10	11	10	11
Penta D	9	14		
D19S433	15	15.2		
vWA	15	17	15	17
D21S11	28	32.2		
D18S51	13			
D6S1043	11	18		
D8S1179	10	11		
D5S818	11	12	11	12
D12S391	18	21		
FGA	18	24		

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.

*Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, **please do not publish** the allele calls from all the STR loci tested.*

Explanation of Test Results

Cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- The submitted sample profile is human, but not a match for any profile in the ExPASy STR database.
- The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (8 core loci plus Amelogenin): U-87MG ATCC
- The submitted profile is similar to the following ExPASy human cell line(s):

e-Signature Technician:



e-Signature Reviewer:



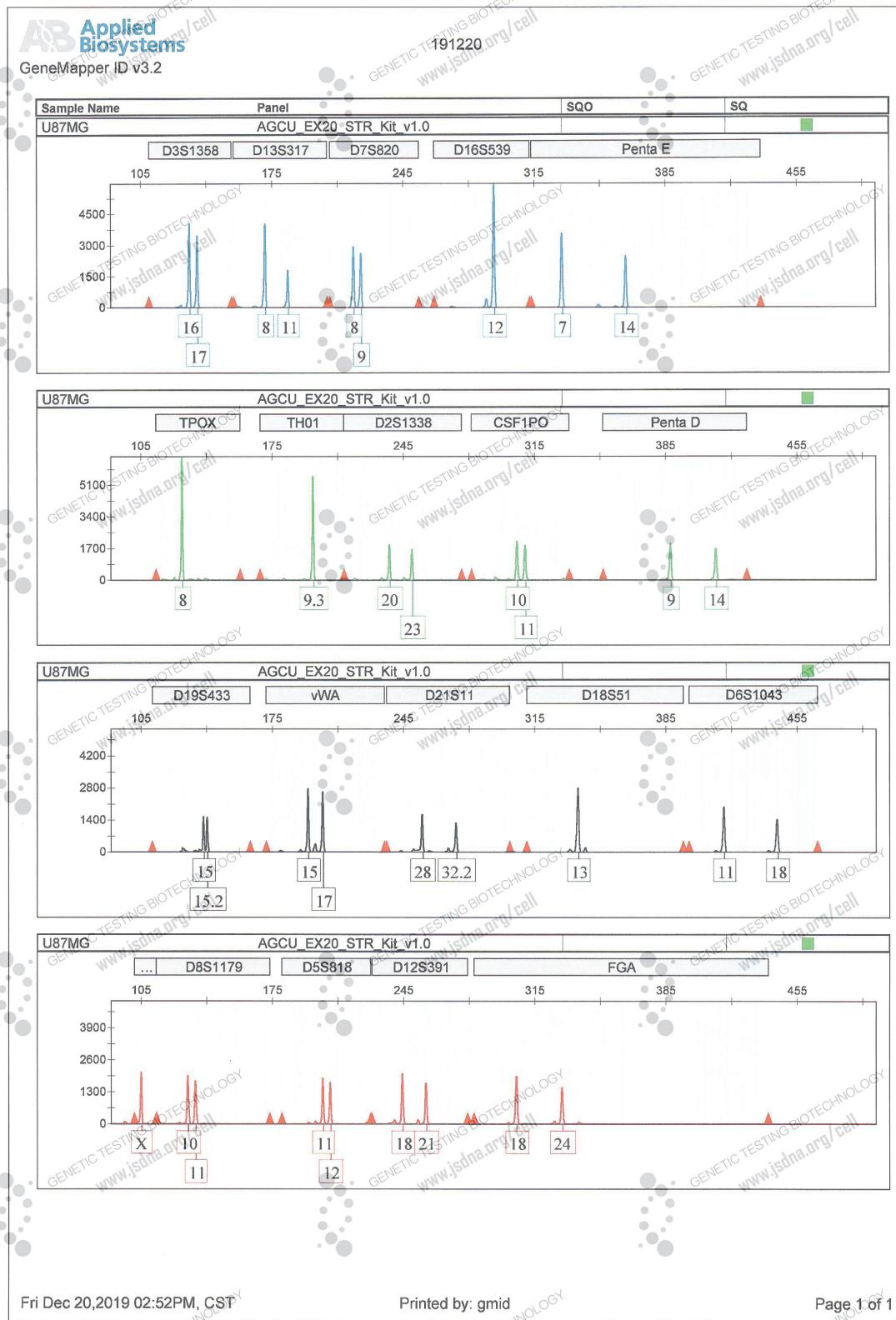
More information

Addendum: Electropherogram for the customer's sample set 1 of 1



GENETIC TESTING BIOTECHNOLOGY

Cell Line Authentication Service STR Profile Report





Cell Line Authentication Service
STR Profile Report

Sample Submitted By: Dr. Zhuohao Liu
Shenzhen Hospital, Southern Medical University
Email Address: lchouhoo@gmail.com
Sales Order: 191220C
Cell Line Designation: U-251MG
Date Sample Received: Dec 20th, 2019
Report Date: Dec 20th, 2019

Methodology: Nineteen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available EX20 Kit from AGCU. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

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GTB™ performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards.

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NOTE: According to the recommendations of IJC on cell line authentication, the report is valid for 3 years since the issue date.

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GENETIC TESTING BIOTECHNOLOGY

Cell Line Authentication Service
STR Profile Report

Sales Order: 191220C

Test Results for Submitted Sample			ExPASy Reference Database Profile	
Loci	Query Profile: U-251MG		Database Profile: U-251MG	
Amelogenin	X			X
D3S1358	16	17		
D13S317	10	11	10	11
D7S820	10	12	10	12
D16S539	12		12	
Penta E	7	10		
TPOX	8		8	
TH01	9.3		9.3	
D2S1338	22	24		
CSF1PO	11	12	11	12
Penta D	12			
D19S433	13	15		
vWA	16	18	16	18
D21S11	29			
D18S51	13			
D6S1043	12			
D8S1179	13	15		
D5S818	11	12	11	12
D12S391	17	22		
FGA	21	25		

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.

*Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, **please do not publish** the allele calls from all the STR loci tested.*

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Cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- The submitted sample profile is human, but not a match for any profile in the ExPASy STR database.
- The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (8 core loci plus Amelogenin): U-251MG
- The submitted profile is similar to the following ExPASy human cell line(s):

e-Signature Technician:



e-Signature Reviewer:



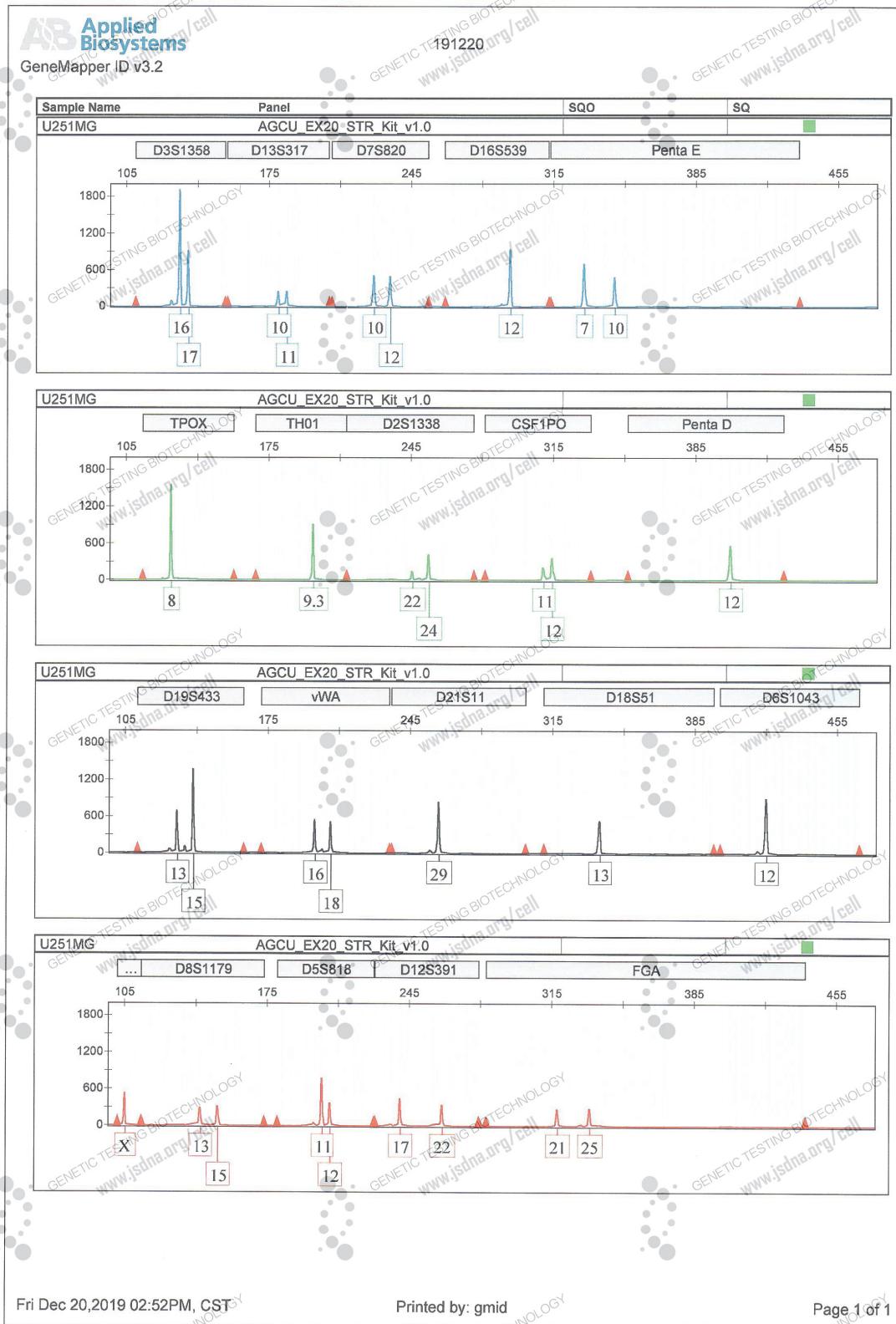
More information

Addendum: Electropherogram for the customer's sample set 1 of 1



Cell Line Authentication Service

STR Profile Report



Transcription Factor/Cis-element	Description	Normal 1	Normal 2	Normal 3	Normal 4	Normal 5	GBM 1	GBM 2	GBM 3	GBM 4	GBM 5	FC	Log2(FC)	p	-Log10(p value)	
SRE	SREBF: sterol regulatory element binding transcription factor	0.03432716	0.026776	0.011079	0.012369	0.028163	0.036478	0.035703	0.048179	0.04125	0.038815	1.778173	0.830395	0.008993	2.046079524	
NF_E1	Nuclear Factor-one family	0.03598074	0.088051	0.120074	0.09794	0.360243	0.048583	0.020698	0.375726	0.085284	0.011680	3.165582	1.662471	0.009414	2.026226309	
E2F-1	E2F1: E2F transcription factor 1	0.75587716	0.385952	0.72903	0.825775	0.616765	0.904046	0.884607	0.827557	0.886921	0.924143	1.176405	0.234384	0.014504	1.838516813	
NF_A3	Nuclear factor A3	0.75038984	0.683264	0.448053	0.809892	0.652805	0.816039	0.978576	0.696777	0.927296	0.840595	1.273555	0.348862	0.047896	1.319699055	
HOXD8,9,10	homeo box D8, 9, 10	0.62438069	0.661657	0.667433	0.79864	0.38368	0.837272	0.962753	0.657536	0.812633	0.807263	1.303486	0.382375	0.04958	1.304693906	
c-Myb	MYB: v-myb myeloblastosis viral oncogene homolog (avian)	0.57657989	0.556731	0.447375	0.714104	0.697528	0.75574	0.73348	0.580704	0.796552	0.868008	1.24801	0.319664	0.061417	1.211713737	
NF_E2	NFE2: nuclear factor (erythroid-derived 2),	0.77625578	0.812351	0.733066	0.847025	0.315214	0.883395	0.968955	0.816467	0.915992	0.951992	1.301467	0.380139	0.071095	1.148163726	
HFH-2	forkhead box D3	0.33432398	0.633074	0.41013	0.879635	0.085436	0.120185	0.989008	0.288259	0.988906	0.926176	1.801681	0.849351	0.089359	1.048862011	
P1F-1	pancreas specific transcription factor	0.13265654	0.411235	0.035539	0.696859	0.396834	0.805093	0.125247	0.133477	0.176897	0.097636	0.369455	1.436553	0.110171	0.958174617	
CBF	impaired CCAAT-binding factor, CP1 (human, rat); NF-Y	0.07389066	0.202068	0.021155	0.261673	0.376016	0.02201	0.204834	0.017024	0.013271	0.017864	0.294448	-1.76376	0.113064	0.94667487	
Ahr/Arnt	aryl hydrocarbon receptor/aryl hydrocarbon receptor nuclear translocator/binding element	0.62153285	0.548573	0.759016	0.880098	0.348823	0.940264	0.965837	0.618903	0.710367	0.91463	1.314105	0.394081	0.121013	0.917169438	
NF_E1 (YY1)	YY1 transcription factor	0.84865554	0.909712	0.674742	0.755432	0.358777	0.837758	0.913807	0.788741	0.952215	0.899162	1.238037	0.308054	0.131885	0.879805119	
TFEB	TFEB is closely related to TFE3 leucine zipper; essential for dimerization; free in solution; tetramerization;	0.63849739	0.544339	0.281411	0.869337	0.14443	0.685503	0.917864	0.745774	0.639484	0.850153	1.468425	0.554269	0.132267	0.878549282	
MRE	Metal response factor	0.76833396	0.874778	0.710232	0.913689	0.506107	0.808674	0.935598	0.803831	0.805264	0.914914	1.152043	0.204194	0.176062	0.754335141	
Tat	transactivating regulatory protein	0.487575139	0.688803	0.234902	0.590256	0.793317	0.342631	0.541519	0.374794	0.515859	0.100577	0.672071	-0.57332	0.17704	0.751929539	
NfkBp65	NFKBp65	0.05567063	0.091974	0.042886	0.072413	0.318353	0.044634	0.031998	0.021952	0.040303	0.349276	-1.51756	0.179735	0.745367036		
MEF-1	MEF-1Myocyte enhancing factor1	0.82614844	0.886142	0.534494	0.934494	0.770203	0.091382	0.999428	0.805558	0.930909	0.176363	0.102504	0.182702	0.738256312		
Sp1	SP1: Sp1 transcription factor	0.60493578	0.641232	0.760316	0.861818	0.64769	0.945667	0.96349	0.585299	0.735879	0.90174	1.175224	0.232936	0.192623	0.715291656	
TEF1(1)	activator; function depends on a highly limiting cofactor; interference with TEF1 / TEIID interaction by a B-cell specific factor	0.43636218	0.690799	0.284336	0.450633	0.386799	0.166691	0.434275	0.389877	0.465241	0.08195	0.68394	-0.54806	0.200884	0.697054319	
ISRE (TRANSFAC)	ISRE (TRANSFAC) interferon-a stimulated response element	0.95690398	0.981447	0.957025	0.98899	0.786293	0.985222	1.040529	0.95355	1.006455	0.963974	1.05975	0.083724	0.206689	0.684682171	
CREB1	CREB1: CAM response element binding protein 1	0.2973081	0.230899	0.268572	0.592299	0.552193	0.63692	0.679841	0.241228	0.451626	0.752473	1.422824	0.508757	0.20725	0.6835046	
ADD1	sterol regulatory element binding transcription factor	0.75577793	0.628989	0.802193	0.910638	0.132115	0.868537	1.01485	0.788378	0.667545	0.83809	1.290973	0.368459	0.238065	0.623305292	
Stat5b	MGF: signal transducer and activator of transcription 5; mammary gland factor; STF-ESR: estrogen receptor	0.1290101	0.134193	0.034401	0.211763	0.801396	0.050752	0.20061	0.073662	0.048338	0.040412	0.31674	-1.66349	0.238801	0.621964549	
ERE	ERBP: ERBP28851	0.852323	0.564339	0.639327	0.200391	0.7474757	0.749303	0.609722	0.945002	0.867863	0.266383	0.340714	0.236361	0.620457885		
ISGF	Interferon-Stimulated Response factor	0.40863374	0.907742	0.771395	0.885555	0.724233	0.63703	0.1413	0.205927	0.172419	0.230334	0.573987	0.626245	0.240168	0.195026894	
Lactoferrin BP	lactoferrin BP	0.6621375	0.259824	0.586767	0.645553	0.294862	0.787233	0.97281	0.560512	0.424178	0.85159	1.357684	0.441126	0.240811	0.618323943	
p53	TP53: tumor protein p53	0.71425599	0.814936	0.473217	0.704215	0.654349	0.724376	0.877534	0.590494	0.887797	1.165829	0.221356	0.245201	0.610477263		
Mfh-1	Mesenchyme fork head 1, Fkh-14; Fork head homologue 14;	0.36939207	0.32088	0.072919	0.746474	0.805889	0.04113	0.092326	0.123043	0.049417	0.450194	-1.15138	0.248726	0.604278264		
HDX8	homeo box D8	0.03729748	0.290928	0.034934	0.30733	0.831947	0.32853	0.024362	0.015457	0.065829	0.340796	-1.55302	0.252370	0.597544645		
AP-1	Fos, FosB, Fra1, Fra2, Jun, JunB	0.65521695	0.697493	0.516692	0.835147	0.558102	0.746843	0.885881	0.645144	0.628804	0.813763	1.140198	0.189284	0.253939	0.59527005	
ATF/CRE	ATF/CRE	0.03891869	0.173019	0.021534	0.484066	0.938048	0.040297	0.385094	0.189183	0.033443	0.052431	0.320251	-1.64273	0.262025	0.581657125	
Fkh	forkhead box O1mouse	0.92141319	0.81598	0.843502	0.827682	0.137129	0.948293	0.918601	0.789044	0.874149	0.90439	1.249159	0.320957	0.262615	0.580682001	
TTF1	trαT/EPB: thyroid-specific enhancer-binding protein, thyroid nuclear insrcriptional intermediary factor 1	0.0655615	0.267764	0.026654	0.481827	0.830761	0.074962	0.424251	0.049482	0.021265	0.110562	0.406873	-1.29735	0.264825	0.577040528	
dax2	Pax-2DNA-binding transcription factor	0.68326662	0.575816	0.600203	0.875712	0.731874	0.812253	0.984208	0.631932	0.687884	0.840305	1.141254	0.19062	0.264876	0.576956648	
PBGD binding protein	porphobilinogen deaminase	0.20017541	0.130831	0.334638	0.754315	0.109866	0.526265	0.987225	0.060724	0.230311	0.712823	1.795269	0.8442	0.276961	0.553322016	
MSP1	the sequences are same as SAA except SP1 binding site is removed	0.86813107	0.969678	0.643678	0.868694	0.017005	0.786132	0.1005597	0.860616	0.98218	1.308519	0.387934	0.281133	0.55108833		
PRDI-BF1	alpha-A-crystallin binding protein I	0.57942773	0.718665	0.051947	0.959474	0.310562	0.88977	0.501395	0.357947	0.174647	0.680938	-0.5544	0.283834	0.546935984		
Pax8	paired box gene 8	0.99080244	0.986367	0.950984	0.978198	0.416199	0.696169	0.161425	0.110516	0.993559	0.970111	1.493952	0.200819	0.284577	0.545800114	
v-Maf	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	0.05273092	0.078694	0.027169	0.663777	0.680161	0.023693	0.048007	0.045482	0.03616	0.039319	0.207889	-2.26611	0.287883	0.540742959	
IT-LF	IT-LF	0.44227221	0.470019	0.255326	0.713805	0.0254	0.563351	0.856767	0.450549	0.418432	0.424311	1.422514	0.508442	0.288082	0.540483508	
EBP40, 45	EBP40, 45	0.95436988	0.913168	0.851655	0.981799	0.515457	0.895149	0.092129	0.928490	0.116145	0.161107	0.289068	0.8442	0.276961	0.553322016	
WT1 (2)	Wilms tumor 1	0.88937161	0.945185	0.885189	0.88176	0.218238	0.960249	0.101531	0.809589	0.964158	0.873273	1.207147	0.271601	0.292687	0.528287132	
E4BP4	nuclear factor, interleukin-3 regulated	0.453834	0.452522	0.452244	0.093834	0.843454	0.992656	0.635353	0.252528	0.635353	0.846441	1.392073	0.4774778	0.52712904		
E47	E2A immunoglobulin enhancer-binding protein E47/helix-hairpin-helix	0.9267203	0.980203	0.987468	0.592458	0.197548	0.821424	0.022238	0.957154	0.191309	0.022108	0.030604	0.423599	-1.23923	0.3178	0.496617468
ODC	ODC (ornithine decarboxylase)	0.44077173	0.62227	0.504719	0.819529	0.568272	0.609867	0.986914	0.518757	0.766918	1.199644	0.282607	0.299831	0.523213679		
MSF-2a	MSF-2a	0.08785428	0.075908	0.028306	0.321445	0.951989	0.03337	0.34215	0.041028	0.029915	0.047933	0.308084	-1.6987	0.301242	0.52082186	
RB	retinoblastoma tumor suppressor protein	0.06834881	0.585804	0.035159	0.410286	0.320206	0.051917	0.488718	0.062057	0.035036	0.035982	0.4747457	-1.07474	0.307082	0.512745535	
Pax4	Pax4	0.95878044	0.960931	0.970371	0.991905	0.520684	0.971272	0.1020917	0.97367	1.002521	0.961614	1.128242	0.154249	0.309616	0.509176798	
Stat1/Stat3	Stat1/Stat3	0.27706702	0.635845	0.077009	0.671196	0.889413	0.231587	0.842367	0.159748	0.134336	0.086598	0.570326	-0.81014	0.310211	0.508342849	
GATA-1	GATA binding protein 1 (globin transcription factor 1)	0.94263417	0.948101	0.988988	0.040188	0.607522	0.993961	0.135601	0.951489	0.989281	0.916155	1.087804	0.121419	0.332135	0.47865696	
HoxA4	HoxA4: Hox-14: Hox-14 (mouse)	0.08448584	0.064761	0.032424	0.138586	0.591761	0.086841	0.187669	0.043934	0.23326	0.021					

Transcription Factor/Cis-element	Description	Normal 1	Normal 2	Normal 3	Normal 4	Normal 5	GBM 1	GBM 2	GBM 3	GBM 4	GBM 5	FC	Log2(FC)	p	-Log10(p value)	
NFIL-2	5' upstream activating sequences (UAS) of the human IL-2 gene	0.26996274	0.918056	0.085975	0.828063	0.425892	0.067971	1.005128	0.112539	0.159442	0.083983	0.565305	-0.8229	0.388851	0.410216455	
YB1	DbpB; FFA1 (rat, chick); CREB-B	0.79662892	0.960306	0.279244	0.733556	0.261286	0.105549	0.783531	0.6126	0.524383	0.118332	0.707483	-0.49923	0.393524	0.405028753	
CREB(2)	ATF-47 (human); CREB-341; CREBalpha; CREB-B	0.03784868	0.077776	0.021616	0.041328	0.363972	0.030555	0.154648	0.012969	0.008244	0.020261	0.417804	-1.2591	0.394274	0.40420139	
SIF3	Si promoter 3	0.03601136	0.454233	0.010456	0.751727	0.897979	0.016831	0.949276	0.01209	0.006807	0.018844	0.466818	-1.09907	0.403973	0.393647892	
Stat4	STAT14: signal transducer and activator of transcription 4	0.79105573	0.927583	0.504638	0.789568	0.015573	0.643231	0.719265	0.678414	0.918928	0.810604	1.24502	0.316169	0.408826	0.388461346	
PARP	poly(ADP-ribose) synthetase/polymerase	0.54216087	0.870232	0.799647	0.899577	0.228778	0.939099	1.023499	0.430247	0.859223	0.788237	1.209529	0.274445	0.414844	0.382114934	
CCAAT	CCAAT binding protein	0.59287075	0.519275	0.516448	0.806378	0.202644	0.799014	0.969927	0.345707	0.512861	0.626153	1.233562	0.30283	0.422181	0.374501507	
PO-B	Stimulatory factor, binds at -15 in propiomelanocortin (POMC) gene; unusual location for a promoter binding site; candidate factor cloned using PO-B binding site, is a phosphoprotein that resembles DNA ligases and repair enzymes	0.06850121	0.072545	0.02809	0.275376	0.864868	0.070042	0.448657	0.030725	0.018361	0.023093	0.451266	-1.14795	0.441503	0.355006639	
CREB-BP1	cAMP response element binding protein	0.02633484	0.021483	0.016198	0.035858	0.285807	0.05347	0.0526	0.017908	0.018142	0.080317	0.446607	-1.16292	0.442687	0.353903501	
TREB-2	transferrin receptor (TR) binding protein	0.06524246	0.085622	0.01989	0.706589	0.37049	0.084382	0.593181	0.07339	0.031394	0.767444	0.530405	0.015653	0.456395	0.340055041	
NF1(2)	CTF, NF-1; TGGCA-binding protein	0.22353861	0.333853	0.02101	0.652059	0.035562	0.101088	0.875422	0.63415	0.044985	0.663129	0.496693	0.572077	0.84277	0.33374527	
NF1(3)	neural fibromatosis 1	0.244655	0.57426	0.089267	0.282615	0.029166	0.027372	0.282615	0.029166	0.027372	0.04563	0.314765	0.528361	0.574149	0.3202467	
NFE-3	neural zinc finger factor 3	0.2777268	0.693564	0.291408	0.831605	0.182259	0.550388	0.98166	0.303194	0.614065	0.595558	1.256524	0.329987	0.466416	0.311226168	
PBPB2	polyoma enhancer binding protein	0.91783042	0.393134	0.826139	0.87247	0.988859	0.864979	1.01314	0.804674	0.887326	0.691377	0.93706	-0.93797	0.486736	0.32971688	
CPE	Cap proximal element	0.05518088	0.164208	0.028767	0.340107	0.717871	0.032367	0.547386	0.026088	0.045247	0.035837	0.525294	-0.92707	0.469025	0.328803925	
Surf-2(2)	Surflet	0.897558935	0.937048	0.804279	0.519375	0.157909	0.863354	0.950576	0.7123	0.942066	0.806537	1.156983	0.210381	0.470165	0.327479489	
REX1,2,3	Regulatory Factor X (RXF)	0.28995884	0.898748	0.075276	0.784147	0.989244	0.192908	0.96349	0.386492	0.381304	0.262575	0.72606	-0.47272	0.473589	0.328409528	
ARE	androgen receptor	0.97931529	0.1002308	0.977801	0.103328	0.681734	0.977228	1.059605	0.959162	1.007109	0.925087	1.054722	0.076863	0.473649	0.35445357	
CEF2	cTnC (Slow/Cardiac Troponin C)	0.95355962	0.9952	0.975688	1.018277	0.745818	0.082104	0.363975	0.102788	0.956276	0.140251	0.060157	0.474043	0.34218182	0.27430242	
MvoD	myoigenic factor D	0.26500323	0.225918	0.445886	0.585393	0.690967	0.665555	0.95633	0.493633	0.263675	0.738203	1.253376	0.325819	0.477006	0.324716228	
SP1, ASP	SP1, ASP	0.22958511	0.707581	0.12639	0.734401	0.214553	0.139405	0.927385	0.043937	0.030539	0.060564	0.591913	-0.739	0.480374	0.318420469	
SRF(2)	serum response factor; CArG-binding factor; CBF(3) (mouse); p67; p65TSRE	0.16612385	0.167726	0.032635	0.545195	0.025254	0.142512	0.546331	0.053391	0.112885	0.645949	-0.6306	0.484895	0.314351576	0.274302309	
ZNF174	zinc-finger protein 174	0.04562664	0.569112	0.018934	0.708442	0.516176	0.038582	0.962853	0.02012	0.030391	0.02538	0.54397	-0.8784	0.486669	0.312766737	
HIF-1	hypoxia-inducible factor 1	0.10420635	0.190859	0.685159	0.89451	0.051737	0.151514	0.013018	0.05736	0.046082	0.924687	1.342348	0.424759	0.489007	0.310684599	
SIE	serum inducible element responsive factor	0.10840155	0.06526	0.282111	0.538526	0.062204	0.084072	0.0519401	0.594673	0.1397543	0.482893	0.483593	0.310372432	0.27430242		
Pur-1	MYC-associated zinc finger protein (purine-binding transcription factor)	0.01895496	0.027648	0.02083	0.352775	0.465389	0.100241	0.310536	0.017484	0.012397	0.045641	0.549119	-0.86481	0.493225	0.306954814	
TFE3-L	TFE3-L is an approximately 3-fold stronger activator than TFE3-S; cooperating with ITF-1, TFE3 can mediate lymphoid-specific activation through combined elements (such as mTF-E, and mTF3 in the IgH enhancer)	0.547091	0.538423	0.104612	0.944556	0.400076	0.465018	0.975391	0.54521	0.540309	0.590533	1.229491	0.298061	0.495322	0.3051112758	
p300	coactivator	0.025998	0.025811	0.018067	0.034082	0.321541	0.026056	0.14211	0.011151	0.011772	0.007806	0.467439	-1.09715	0.502429	0.298925061	
MUSF1	In the sequence, it is the same as SAA except USF binding site is removed	0.7805218	0.844359	0.823403	0.92297	0.878932	0.875239	0.137378	0.738229	0.926484	0.863724	1.044685	0.063068	0.503231	0.298230309	
HOXA9	homeobox protein	0.01007461	0.054231	0	0.063613	0.321142	0.018768	0.130237	0.014009	0.036329	0.052114	0.497474	-1.00731	0.502617	0.297809288	
EGR2, BP	early growth factor 2 binding protein	0.10215468	0.1838901	0.244139	0.343829	0.158575	0.556513	0.939587	0.099495	0.043988	0.490756	1.507804	0.592449	0.504083	0.29748907	
ICSBP	interferon consensus sequence binding	0.12856134	0.836295	0.071917	0.844164	0.572745	0.123545	0.071	0.08951	0.307236	0.167676	0.672167	0.572111	0.507701	0.29431982	
PREB	a Growth Hormone Gene Promoter	0.08917099	0.149232	0.080593	0.623728	0.759447	0.0340413	0.582888	0.052753	0.0662	0.06794	0.637887	-0.64863	0.50781	0.29428498	
Myc/Max	myc-associated factor X	0.00869662	0	0.030548	0.033237	0.608347	0.134525	0.029278	0.125079	0.010636	0.032756	0.059511	0.349471	-1.151676	0.508114	0.294038485
ALF18	murine leukemia virus	0.44777291	0.757522	0.107564	0.610797	0.631732	0.169345	0.782794	0.629442	0.262167	0.097153	0.762927	-0.39038	0.508918	0.29355011	
Mvb2	Mvb2	0.14664831	0.411602	0.632328	0.846266	0.654639	0.308188	0.103224	0.779632	0.58618	0.794954	1.26389	0.337642	0.509442	0.292905206	
N-ras binding protein	N-ras promoter region	0.17194201	0.207092	0.371504	0.585393	0.070833	0.020536	1.01381	0.075117	0.168591	0.644852	1.449895	0.535948	0.512298	0.290477009	
SSAP	New activator of sea urchin H1 gene; related to several RNA-binding protein and keratinocyte transcriptional protein-1	0.09768388	0.084602	0.036974	0.227755	0.015788	0.086864	0.817899	0.047512	0.02573	0.02803	2.175573	1.121395	0.513323	0.289069579	
KTP1	keratinocyte transcriptional protein-1	0.01267747	0.023507	0.014736	0.017626	0.64485	0.0141824	0.030138	0.011454	0.101547	0.120549	0.390403	-1.35696	0.514864	0.288307544	
HLF	hepatocyte nuclear factor	0.02103725	0.127655	0.01953	0.233969	0.346594	0.035419	0.007678	0.055648	0.01594	0.579317	0.78757	0.515105	0.288104227	0.274301988	
EKL(F1)	erythroid Kruppel-like factor gene	0.16771619	0.827359	0.069181	0.857486	0.74052	0.205984	0.989803	0.168824	0.314824	0.205474	0.073761	-0.49948	0.518138	0.285554483	
AP3	activator protein 3	0.03187741	0.062426	0.013926	0.233674	0.538485	0.025735	0.030328	0.012085	0.021085	0.047456	0.548542	-0.86632	0.519239	0.286348023	
PPUR(1)	purine-rich sequences binding sequence	0.26665637	0.291489	0.851465	0.3639874	0.936874	0.134525	0.029278	0.125443	0.028826	0.010558	0.073735	-0.419968	0.519866	0.28410854	
H4T-1	Histone H4 transcription factor 1	0.05361898	0.076998	0.0205056	0.3636661	0.949636	0.059944	0.720003	0.020332	0.013864	0.026798	0.571691	-0.80669	0.587474	0.231036804	
CEF1	RUNX1-related transcription factor 1	0.06577586	0.129599	0.156646	0.524054	0.578237	0.206146	0.513694	0.072442	0.073351	0.210957	0.740075	-0.43426	0.589068	0.229843043	
AML1	acute myeloid leukemia 1: aml1 oncogene	0.35270131	0.098948	0.582623	0.021494	0.640933	0.940928	0.155597	0.130703	0.543192	1.319381	0.399861	0.590209	0.228994013	0.27430242	
NF-Y	NF-Y, also known as CBF (CCAAT-binding factor), was first identified as a protein that binds to the Y box of MHC (major histocompatibility complex) class II E	0.07095096	0.933063	0.019395	0.794418	0.072157	0.018255	1.024974	0.016454	0.028666	0.010856	0.581595	-0.78191	0.592304	0.227455362	
NF-4FA	0.16153056	0.367949	0.576393	0.772133	0.											

Transcription Factor/Cis-element	Description	Normal 1	Normal 2	Normal 3	Normal 4	Normal 5	GBM 1	GBM 2	GBM 3	GBM 4	GBM 5	FC	Log2(FC)	p	-Log10(p value)		
NF-Atx	NFATx, a novel member of the nuclear factor of activated T cells family that is expressed predominantly in the Thymus	0.05089361	0.037425	0.033372	0.409087	0.90023	0.100014	0.760567	0.021423	0.009899	0.02233	0.638874	-0.646396	0.655548	0.183395647		
NFAT-1	nuclear factor of activated T-cells	0.057847483	0.072888	0.033913	0.482045	0.144213	0.251072	0.900464	0.027332	0.017612	0.02941	1.549985	0.632254	0.657248	0.18226895		
ATF-1delta		0.188181197	0.194066	0.164366	0.804601	0.580972	0.407308	0.891648	0.315557	0.065357	0.694741	1.230245	0.294045	0.680297	0.18026728		
HFF-8, HNF3.LUN	a new mouse forkhead gene named LUN	0.034847731	0.690683	0.014221	0.639811	0.093358	0.026653	0.876595	0.019241	0.011991	0.016357	0.845591	-0.631295	0.660986	0.179808029		
ABF-1	MCL-2 (myc/mi light chain-2),	0.032275349	0.142767	0.129272	0.70316	0.076598	0.517971	0.965904	0.080291	0.008431	0.062422	1.453876	0.539905	0.673531	0.171642643		
Stat5	STAT5: signal transducer and activator of transcription 5	0.283895703	0.36419	0.056342	0.343567	0.122795	0.382579	0.78179	0.2038	0.318977	0.070791	1.156401	0.209646	0.675199	0.170562829		
MTF	MRE-binding transcription factor-1	0.519868122	0.476668	0.428793	0.727671	0.549285	0.637082	0.948605	0.469184	0.336861	0.548086	1.088494	0.122334	0.687223	0.162902194		
Skn	octamer-binding site in epidermis (POU domain factor)	0.253947478	0.790027	0.38307	0.907369	0.277065	0.712076	1.018805	0.027877	0.727323	0.567622	1.169339	0.225693	0.688251	0.162253315		
MEF-3	myelin gene expression factor 3	0.098970005	0.113613	0.073705	0.508689	0.452135	0.473337	0.813234	0.121478	0.153696	0.383996	1.285358	0.360149	0.692068	0.159851147		
DE-1	Ref-1 element from albumin gene	0.061182571	0.254988	0.091626	0.694925	0.734729	0.310045	0.92249	0.022968	0.007693	0.114919	0.75032	-0.414421	0.693112	0.159196751		
Tax/CREB	TAX: transactivating responsive element	0.100194861	0.205742	0.268362	0.507666	0.308413	0.356329	0.950663	0.03221	0.095084	0.138011	0.324876	0.409772	0.696029	0.157372704		
NFKB	nuclear factor of kappa light polypeptide gene enhancer in B-cells	0.223366814	0.326454	0.151879	0.433606	0.230122	0.447281	0.045861	0.194988	0.288694	0.609523	1.161979	0.216584	0.696548	0.157048663		
E2	BPV-1: bovine papilloma virus type 1	0.482993345	0.900745	0.210469	0.929872	0.810226	0.348917	0.980923	0.672263	0.154414	0.588101	0.875669	-0.191543	0.699791	0.155031676		
SIF1	Surfactant-isomaltase (S1) is an enzyme-specific gene which exhibits a complex pattern of expression during intestinal development and in the adult intestinal mucosa Sf1/S1 is	0.022078395	0.079613	0.017173	0.23146	0.790502	0.118367	0.606422	0.021847	0.007369	0.026796	0.684417	-0.547052	0.707648	0.15018262		
C/EBPalpha(1)	CCAAT/enhancer binding protein alpha	0.514784885	0.787505	0.346627	0.858167	0.22458	0.639801	0.969994	0.540907	0.191605	0.729816	1.124552	0.16935	0.710147	0.148651644		
Smad 3/4	Mad-1: Mad-2: mothers against decapentaplegic homologs 3/4	0.640916522	0.83726	0.671903	0.875985	0.282959	0.983638	0.232017	0.865999	0.025091	0.93078	-0.103534	0.715225	0.145557302			
Freac-7	forkhead box L1	0.024987476	0.055296	0.036243	0.366323	0.560063	0.131961	0.552482	0.015878	0.282135	0.033515	0.730679	-0.452691	0.71598	0.14509916		
ACF	albumin caac-binding factor	0.040390299	0.113768	0.019449	0.678905	0.472723	0.030846	0.862615	0.015363	0.009149	0.020406	0.705212	-0.503872	0.724068	0.142022057		
MZF1(1)	myeloid zinc finger 1	0.771182161	0.834022	0.086522	0.954146	0.392122	0.947871	0.261214	0.420278	0.167172	0.713838	0.923381	-0.115002	0.725195	0.139545016		
Pit 1	POU domain class 1, transcription factor 1 (Pit-1, growth hormone factor 1)	0.069756705	0.238372	0.275343	0.673403	0.309323	0.492498	0.925909	0.049088	0.152291	0.275878	1.210361	0.275437	0.729865	0.136757473		
URE		0.374781524	0.461425	0.081939	0.124557	0.450645	0.811767	0.945219	0.047065	0.088603	0.263166	0.205813	0.054827	0.844375	-0.244045	0.731098	0.13602459
Freac-2 (2)	forkhead box F2; Fork head BE1related	0.575823928	0.840965	0.086219	0.954638	0.741533	0.884496	0.103251	0.134204	0.862563	0.578355	0.924224	-0.113686	0.731123	0.13600962		
RSRC4	RS response transcription element	0.056457221	0.147613	0.154262	0.495872	0.482996	0.860803	0.102649	0.016029	0.130745	0.678039	0.202647	0.266213	0.731184	0.135973394		
Pax-6	pax-6 plays an essential role in the development and function of glucagon-producing cells in both pancreatic and	0.111371779	0.073479	0.613259	0.866941	0.454146	0.876339	0.998807	0.026908	0.087434	0.575034	1.207665	0.27222	0.732984	0.134905626		
CD28RC	T-cell accessory molecule CD28	0.057385454	0.196812	0.073407	0.468941	0.620148	0.128465	0.851787	0.015817	0.024856	0.054646	0.764481	-0.387448	0.743788	0.128550885		
AF1, ARP1., NF-BA	NF2R2: nuclear receptor subfamily 2, group F, member 2	0.168267381	0.262595	0.190424	0.742791	0.880536	0.48596	0.941197	0.148294	0.084655	0.218836	0.837088	-0.256548	0.745305	0.127665824		
Beta-response element	Beta-response element	0.796996583	0.936208	0.067435	0.807495	0.210745	0.106455	0.635287	0.230166	0.027338	0.092599	0.147426	0.066629	0.747245	0.126537177		
HNF-1α/b/c	hepatocyte nuclear factor-1	0.04173765	0.030264	0.042020	0.543588	0.773556	0.20945	0.81377	0.017726	0.034204	0.019208	0.744466	-0.425722	0.74806	0.126045936		
NKX-2.5	conservation homeobox	0.040276002	0.027402	0.042420	0.542005	0.010053	0.356337	0.027402	0.027402	0.016029	0.027402	0.750345	-0.402016	0.731016	0.134745016		
X2R	X2 binding protein X2BP	0.031989893	0.127188	0.01758	0.337737	0.042437	0.104416	0.62	0.020665	0.004309	0.01899	1.379544	0.464296	0.757918	0.12079032		
CTCF	CCCTC binding factor	0.932008373	0.97055	0.860946	0.321045	0.862616	1.01837	0.852283	1.02302	0.852105	0.985298	-0.021368	0.758795	0.198755333			
Sp1; NF-κB; B1	B1 acts as an activator or as a repressor, after phosphorylation at Ser-148 by CK II, PU-1 recruits NF-EM5 to bind to DNA resulting in pronounced transcriptional activation; PU-1 interferes with the commitment of erythroid blast to differentiate; activated by proviral integration of SV40 (anemia- or polythemia-inducing strains) in																
PU.1		0.140983262	0.177316	0.134949	0.846071	0.677366	0.714374	0.975157	0.103418	0.117005	0.427214	1.182367	0.241678	0.759794	0.119304331		
GKLF	gut-enriched Krueppel-like factor; EZF;	0.115168994	0.216422	0.126011	0.340543	0.846055	0.236021	0.773005	0.088419	0.039564	0.213389	0.821311	-0.284	0.7632	0.117361846		
LR1	LR1 is a 106-kDa sequence-specific DNA-binding protein first identified as a potential regulator of immunoglobulin class switch recombination in R lymphocytes	0.033377879	0.62473	0.018067	0.629404	0.018841	0.023596	0.890005	0.015363	0.014114	0.026578	0.732136	-0.449816	0.763988	0.116913526		
TransferrinBP	transferrin binding protein	0.344925165	0.439724	0.216269	0.057028	0.194831	0.610895	0.948841	0.206467	0.138364	0.128356	1.140982	0.200481	0.765781	0.116580534		
FAST-1	FOXP3: forkhead box H1	0.388163299	0.5208	0.011037	0.762597	0.271809	0.090223	0.302709	0.734713	0.014557	0.120224	0.163852	0.76434	0.145525409			
TxREF-NF III	Tax-responsive element (TRE)-binding factor	0.219587161	0.471368	0.053638	0.832698	0.888524	0.629573	0.965574	0.313678	0.178703	0.361988	0.98394	-0.157795	0.768993	0.114586025		
c-Ets-1	c-Ets-1: p55-Ets 1-p54; Ets-1: c-Ets-1 54	0.064122474	0.053624	0.035295	0.165137	0.862822	0.089822	0.165137	0.050824	0.029988	0.295098	0.017537	0.80365	0.31536	0.770165		
ISRE (1)	interferon-a stimulated response element	0.069572974	0.0507007	0.091989	0.779434	0.27071	0.205984	0.974587	0.042725	0.080595	0.091136	0.808705	-0.306315	0.773092	0.111769016		
MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	0.672303977	0.811822	0.807286	0.865768	0.808923	0.829472	0.051727	0.738908	0.739496	0.968148	-0.046701	0.774352	0.111061578			
Brn-3	POU domain class 4, transcription factor 1	0.172891289	0.614144	0.039358	0.792402	0.625753	0.163292	0.893793	0.364918	0.134667	0.230394	0.878842	-0.186324	0.786763	0.104156243		
RFX1/2/3	I, belongs to a novel family of homodimeric and heterodimeric DNA-binding proteins	0.172891289	0.614144	0.039358	0.792402	0.625753	0.163292	0.893793	0.364918	0.134667	0.230394	0.878842	-0.186324	0.786763	0.104156243		
CREB2	2. An IFN/CREB transcription factor that can negatively regulate transcription	0.347129942	0.739277	0.076955	0.468559	0.149181	0.103888	0.623687	0.34701	0.383865	0.115262	0.883883	-0.178072	0.793177	0.100630037		
TFE3	Serum Response Factor	0.029432932	0.129005	0.023759	0.475125	0.009462	0.124747	0.774743	0.009207	0.007713	0.020678	1.320917	0.40154	0.801769	0.095920772		
ORE	osmotic response element	0.114740287	0.339462	0.187718	0.652782	0.327868	0.526483	0.865965	0.073208	0.055302	0.343739	1.144525	0.194749	0.796935	0.098577133		
WT1 (3)	Wilm's tumor 1	0.246276959	0.414722	0.188664	0.580724	0.270428	0.470874	0.858694	0.153797	0.041771	0.89847	-0.157673	0.798653	0.09764161			
AIC, CBF	ApoA-I gene promoter c region, CCAAT-binding factor	0.36106291	0.418116	0.251546	0.161793	0.437455	0.845495	0.263257	0.432111	0.359316	0.121637	0.7988	0.097511303				
Stat5/Stat6	STAT5: signal transducer and activator of transcription 5	0.037052508	0.117909	0.534678	0.79785	0.462399	0.780856	0.906029	0.027029	0.031757	0.473291	1.137993	0.186493	0.821271	0.08551374		
NPAS2	neurofibromatosis protein 2	0.015345176	0.021886	0.052456	0.523972	0.471608	0.469323	0.645932	0.008003	0.012584	0.143939	1.185643	0.245669	0.821928	0.085166205		
TEF1(2)	TEF-1: transcription factor TFIID interaction by TEF-1 /																

Transcription Factor/Cis-element	Description	Normal 1	Normal 2	Normal 3	Normal 4	Normal 5	GBM 1	GBM 2	GBM 3	GBM 4	GBM 5	FC	Log2(FC)	p	-Log10(p value)
LF-A1(2)	Liver-specific transcription factor	0.05720172	0.057818	0.02018	0.312754	0.485002	0.081695	0.617318	0.029816	0.0242	0.073127	0.885524	-0.1754	0.887004	0.052074519
Pax2	paired box gene 2(gene5/gene8)	0.66434228	0.975345	0.491284	0.924886	0.002866	0.34089	1.008916	0.644538	0.529817	0.379867	0.949425	-0.07487	0.888028	0.051573406
Freac-4	forkhead box D1	0.0331329	0.064481	0.163472	0.752327	0.44829	0.438283	0.91726	0.031119	0.054802	0.174538	1.105562	0.144478	0.888983	0.051106575
Isl-1	Islet-1	0.03539223	0.064793	0.098869	0.759628	0.872432	0.54367	0.921317	0.016787	0.005933	0.162375	0.902022	-0.14877	0.892093	0.049589678
HEN1	HEN1 and JEN2 encode a distinct subgroup of bHLH proteins. bHLH protein by HEN1 and HEN2 may severs important regulatory functions in the developing nervous system	0.04516731	0.060216	0.066581	0.720997	0.872986	0.537391	0.874215	0.035392	0.022795	0.458803	1.092103	0.127109	0.897192	0.047114818
PCF	Promoter-linked coupling element	0.14689329	0.249954	0.059728	0.747287	0.37884	0.264731	0.862615	0.069875	0.075505	0.186375	0.921905	-0.11731	0.899715	0.045894881
Stat3	STAT3: signal transducer and activator of transcription 3	0.42230672	0.815714	0.302566	0.709936	0.757919	0.599827	0.490998	0.434853	0.809074	0.752	1.02603	0.037073	0.902689	0.04461898
Lyf-1	LyF-1	0.15926454	0.489447	0.16889	0.667028	0.547729	0.330759	0.842501	0.16702	0.517576	0.1045325	0.063952	0.9095723	0.041090669	
Freac-2 (1)	forkhead box F2 (mouse)	0.01757697	0.077306	0.106633	0.394457	0.207887	0.101016	0.64293	0.015666	0.038408	0.084564	0.1097658	0.134429	0.910178	0.040873527
MHC gene promoter W	MHC class II Ebeta	0.05827349	0.109036	0.820531	0.914479	0.84626	0.827853	0.1016124	0.040301	0.017612	0.683594	0.940661	-0.08825	0.910475	0.040731978
LXRE1	nuclear receptor subfamily 1, group H	0.15016983	0.5312	0.05813	0.746251	0.126534	0.244986	0.92896	0.122962	0.072164	0.12385	0.925968	-0.11097	0.911897	0.04054404
G8BF1/2/3/HY5	G-box binding factor 1	0.3940427	0.490848	0.436378	0.688005	0.58478	0.617144	0.976129	0.177688	0.273948	0.635157	1.033157	0.04706	0.917798	0.039625452
MvT1	myeloid transcription factor 1	0.03195883	0.053768	0.116803	0.784501	0.568193	0.615215	0.864708	0.026948	0.268899	0.1073272	0.108721	0.9162633	0.037970385	
Pax3	paired box gene 3	0.19622518	0.503738	0.120485	0.830733	0.379976	0.297292	0.945689	0.135622	0.316572	0.232851	0.949228	-0.07517	0.9165988	0.037625636
Pax5(2)	Pax5(2) is required for the early stages of B-cell differentiation. Pax-5DNA-binding transcription factor	0.2212739	0.242855	0.078418	0.555983	0.57432	0.428217	0.826811	0.103994	0.066858	0.33557	1.052962	0.074453	0.918828	0.0367655839
LF-A2	liver-specific factors stimulate <i>in vitro</i> transcription from the human alpha1-antitrypsin promoter	0.09097769	0.078866	0.091745	0.645342	0.436821	0.209868	0.917495	0.067481	0.056176	0.191495	1.073498	0.10232	0.922941	0.034826015
p53(2)	Tumor protein p53	0.25578479	0.341897	0.23501	0.743854	0.810468	0.549561	0.862079	0.350888	0.151854	0.542859	1.029421	0.041833	0.936653	0.028421258
GATA	GATA: GATA binding protein (globin transcription factor)	0.07532989	0.104864	0.140719	0.547293	0.668129	0.508681	0.759696	0.102661	0.102485	0.130895	1.044315	0.062557	0.942504	0.025716788
Fra-1/JUN	Fos-related antigen	0.4010245	0.464944	0.787566	0.886283	0.498907	0.844134	1.026147	0.1787147	0.218522	0.845497	1.024449	0.034848	0.942844	0.025560293
bela M-globin factor B1	beta M-globin factor B1	0.05995769	0.057756	0.088251	0.353851	0.642122	0.359599	0.724998	0.021968	0.026869	0.9530	-0.06939	0.951873	0.021420825	
GATA1(2)	GATA1(2)	0.04378933	0.056697	0.050003	0.509288	0.438097	0.174797	0.614032	0.030301	0.019954	0.215786	0.960992	-0.0574	0.955903	0.019586377
EVI-1	ecotropic viral integration site 1(zinc finger oncogene)	0.25486614	0.720596	0.341599	0.752763	0.276475	0.659447	0.94656	0.057421	0.306018	0.428703	1.022099	0.031535	0.957286	0.01895843
EIF-1	EIF-1 like factor 1, a novel Ets family member	0.017846501	0.022199	0.017228	0.383669	0.275442	0.051108	0.679639	0.011242	0.000906	0.015649	0.1057936	0.081252	0.958161	0.018651307
EIK1	member of Ets oncogene family	0.03738935	0.054362	0.202235	0.73549	0.810804	0.0630549	0.937341	0.015635	0.032226	0.188046	0.965503	-0.05065	0.96017	0.017651904
AP2	activator protein 2	0.14827128	0.155708	0.194596	0.443269	0.220794	0.188668	0.664654	0.054512	0.049306	0.173594	0.972644	-0.04002	0.960891	0.017325654
v-rel 50-55K	NF-kappaB 50-55K protein	0.50351602	0.497791	0.860539	0.941693	0.577433	0.967582	0.98597	0.265316	0.237445	0.767469	0.985681	-0.02081	0.961542	0.017031929
SRY	testis determining factor binding domain	0.04639219	0.208358	0.028333	0.626735	0.259935	0.150863	0.913505	0.010363	0.04157	0.101847	0.145257	0.0587	0.96255	0.016563024
Cdx2	caudal type homeobox transcription factor 2	0.03570514	0.357306	0.479339	0.826565	0.521913	0.277274	0.1003518	0.026105	0.510433	0.102542	0.036215	0.962588	0.016559418	
TR	thyroid hormone receptor	0.72194209	0.879417	0.497921	0.875603	0.779848	0.634848	0.939777	0.492696	0.968109	0.574007	1.007184	0.010327	0.963262	0.01625561
CDP	CCAAT displacement protein	0.03916542	0.022324	0.160553	0.519232	0.777838	0.161942	0.726004	0.018908	0.119441	0.584433	1.030415	0.043225	0.968285	0.015344465
HNF-1A	hepatocyte nuclear factor 1	0.23238966	0.77661	0.614294	0.884294	0.555307	0.813152	0.008440	0.151658	0.321381	0.757047	0.988147	-0.02013	0.966058	0.014996723
LSF	Transforming Growth Factor beta1control	0.86182296	0.642384	0.820315	0.77908	0.835687	0.944146	0.95776	0.675986	0.455623	0.886345	0.994383	0.00813	0.967001	0.014572863
TCE	Thy-1binding protein	0.05147543	0.213713	0.043421	0.602515	0.212266	0.233076	0.801098	0.014332	0.022574	0.088413	1.032084	0.04556	0.988884	0.01572827
Thy-1binding protein	Thy-1binding protein	0.81438563	0.9005	0.821723	0.943603	0.335148	0.946091	0.990813	0.854585	0.103265	0.884275	0.998445	-0.01385	0.971528	0.012544666
Pax-5	PAX5: paired box gene 5 (B-cell lineage specific activator protein)	0.8560048	0.946109	0.490851	0.731949	0.568793	0.722499	0.183244	0.794406	0.934572	0.903051	0.992033	-0.01154	0.972771	0.011989512
HINF	histone gene transcription factors	0.43832198	0.984561	0.278648	0.902356	0.477682	0.454887	1.038015	0.149325	0.87646	0.528227	0.988754	-0.01632	0.974443	0.011243614
c-Myc-responsive region	c-myc responsive region	0.03800179	0.06856	0.274504	0.639484	0.60455	0.595263	0.785007	0.04227	0.015882	0.218436	1.019358	0.02766	0.975663	0.01070267
XBP-1	X-box binding protein 1	0.48897062	0.981883	0.187905	0.910121	0.180025	0.326843	1.014313	0.171081	0.782375	0.488105	1.0123	0.017638	0.977226	0.01000482
c-myb binding protein	c-myb binding protein	0.82421926	0.96012	0.757553	0.904598	0.619648	0.694048	0.948002	0.86304	0.763514	0.806964	1.002297	0.00331	0.980339	0.008623682
LF-A1	liver-specific TF	0.66112698	0.945593	0.447619	0.845881	0.429107	0.470747	1.027421	0.406158	0.871995	0.507063	1.005334	0.007675	0.982665	0.007594626
Ets-1/PEA3	Ets-domain transcription factor pea3	0.17779079	0.474471	0.040662	0.206451	0.462753	0.126167	0.185122	0.092449	0.356823	0.615296	1.010524	0.015104	0.982757	0.007553817
RIPE3a1	rat insulin promoter element 3(RIPE3) can confer either positive regulation in insulin-	0.1376761	0.426803	0.128476	0.521521	0.23398	0.259746	0.764758	0.106933	0.034599	0.29799	1.01075	0.015426	0.983942	0.007030395
TTF-1(1)	Thyroid-specific enhancer. Homolog of Drosophila Nk2 factor, and mammalian Nkx family; site in promoters of eight thyroid-specific genes; also regulates pulmonary-	0.23144038	0.36995	0.080639	0.402848	0.336087	0.294703	0.629286	0.233259	0.198474	0.074216	1.006315	0.009082	0.987372	0.005519378
EGF binding protein	epidermal growth factor	0.04280943	0.045644	0.05989	0.624991	0.517354	0.342897	0.883803	0.013999	0.008556	0.029265	0.990572	-0.01367	0.991154	0.003858909
XBP1_X2BP	X-box binding protein 1	0.02973387	0.154525	0.015142	0.526152	0.295956	0.064475	0.871633	0.018544	0.005059	0.053011	0.9914	-0.01246	0.992949	0.003073232
CD28RC_NF-IL2B	I-cell accessory molecule CD28	0.02161907	0.254811	0.021209	0.396991	0.162109	0.020391	0.805389	0.00182	0.008993	0.017283	0.994746	-0.0076	0.996004	0.001738879
ACPBPI(CRY-alphaA)	alphaA-crystallin	0.32030515	0.302915	0.328381	0.644715	0.557216	0.604197	0.844479	0.20926	0.131525	0.365489	1.000658	0.000949	0.99853	0.000638968